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SEQUENCE LISTING

<110> MIYATA, Toshio

<120> A Method for Detecting Megsin Protein and Use Thereof

<130> SHIM-012

<140> 09/936,883

<141> 2001-12-21

<150> JP 1999-75305

<151> 1999-03-19

<150> JP 1999-306623

<151> 1999-10-28

<160> 21

<170> PatentIn Ver. 2.0

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1140)

<300>

<302> A mesangium-predominant gene, megsin, is a new serpin upregulated in IgA nephropathy.

<303> J. Clin. Invest.

<304> 120

<305> 4

<306> 828-836

<307> 1998-08-15

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atg gcc tcc ctt gct gca gca aat gca gag ttt tgc ttc aac ctg ttc 48
Met Ala Ser Leu Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe
1 5 10 15

aga gag atg gat gac aat caa gga aat gga aat gtg ttc ttt tcc tct 96
Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
20 25 30

ctg agc ctc ttc gct gcc ctg gtc cgc ttg ggc gct caa gat 144
Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
35 40 45

gac tcc ctc tct cag att gat aag ttg ctt cat gtt aac act gcc tca 192
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
50 55 60

ggatatggaaac	tctaatagt	cagtcagg	ctccag	tctcaa	ctg		240									
Gly	Tyr	Gly	Asn	Ser	Ser	Gln										
65	70	75	80													
aaaaga	gtt	ttt	tct	gat	ata	aat	gca	tcc	cac	aag	gat	tat	gat	ctc		288
Lys	Arg	Val	Phe	Ser	Asp	Ile	Asn	Ala	Ser	His	Lys	Asp	Tyr	Asp	Leu	
85	90	95														
agcatatt	gtg	aat	ggg	ctt	ttt	gct	gaa	aaa	gtg	tat	ggc	ttt	cat	aag		336
Ser	Ile	Val	Asn	Gly	Leu	Phe	Ala	Glu	Lys	Val	Tyr	Gly	Phe	His	Lys	
100	105	110														
gactacatt	gag	tgt	gcc	gaa	aaa	tta	tac	gat	gcc	aaa	gtg	gag	cga			384
Asp	Tyr	Ile	Glu	Cys	Ala	Glu	Lys	Leu	Tyr	Asp	Ala	Lys	Val	Glu	Arg	
115	120	125														
gttgac	ttt	acg	aat	cat	tta	gaa	gac	act	aga	cgt	aat	att	aat	aag		432
Val	Asp	Phe	Thr	Asn	His	Leu	Glu	Asp	Thr	Arg	Arg	Asn	Ile	Asn	Lys	
130	135	140														
tgggtt	gaa	aat	gaa	aca	cat	ggc	aaa	atc	aag	aac	gtg	att	ggt	gaa		480
Trp	Val	Glu	Asn	Glu	Thr	His	Gly	Lys	Ile	Lys	Asn	Val	Ile	Gly	Glu	
145	150	155	160													
ggtgttgc	ata	agc	tca	tct	gct	gta	atg	gtg	ctg	gtg	aat	gct	gtg	tac		528
Gly	Gly	Ile	Ser	Ser	Ala	Val	Met	Val	Leu	Val	Asn	Ala	Val	Tyr		
165	170	175														
ttcacat	ttc	aaa	tct	ccc	aag	tgc	tct	ggg	aag	gca	gtc	gcc	atg	atg		576
Phe	Lys	Gly	Lys	Trp	Gln	Ser	Ala	Phe	Thr	Lys	Ser	Glu	Thr	Ile	Asn	
180	185	190														
tgcat	ttc	aaa	tct	ccc	aag	tgc	tct	ggg	aag	gca	gtc	gcc	atg	atg		624
Cys	His	Phe	Lys	Ser	Pro	Lys	Cys	Ser	Gly	Lys	Ala	Val	Ala	Met	Met	
195	200	205														
catcag	gaa	cg	aag	ttc	aat	ttg	tct	gtt	att	gag	gac	cca	tca	atg		672
His	Gln	Glu	Arg	Lys	Phe	Asn	Leu	Ser	Val	Ile	Glu	Asp	Pro	Ser	Met	
210	215	220														
aagatt	ctt	gag	ctc	aga	tac	aat	ggt	ggc	ata	aac	atg	tac	gtt	ctg		720
Lys	Ile	Leu	Glu	Leu	Arg	Tyr	Asn	Gly	Gly	Ile	Asn	Met	Tyr	Val	Leu	
225	230	235	240													
ctgcct	gag	aat	gac	ctc	tct	gaa	att	gaa	aaa	ctg	acc	ttt	cag		768	
Leu	Pro	Glu	Asn	Asp	Leu	Ser	Glu	Ile	Glu	Asn	Lys	Leu	Thr	Phe	Gln	
245	250	255														
aatcta	atg	gaa	tgg	acc	aat	cca	agg	cga	atg	acc	tct	aag	tat	gtt		816
Asn	Leu	Met	Glu	Trp	Thr	Asn	Pro	Arg	Arg	Met	Thr	Ser	Lys	Tyr	Val	
260	265	270														
gaggta	ttt	ttt	cct	cag	ttc	aag	ata	gag	aag	aat	tat	gaa	atg	aaa		864
Glu	Val	Phe	Phe	Pro	Gln	Phe	Lys	Ile	Glu	Lys	Asn	Tyr	Glu	Met	Lys	
275	280	285														
caatat	ttg	aga	gcc	cta	ggg	ctg	aaa	gat	atc	ttt	gat	gaa	tcc	aaa		912

Gln	Tyr	Leu	Arg	Ala	Leu	Gly	Leu	Lys	Asp	Ile	Phe	Asp	Glu	Ser	Lys	
290					295				300							
gca	gat	ctc	tct	ggg	att	gct	tcg	ggg	ggt	cgt	ctg	tat	ata	tca	agg	960
Ala	Asp	Leu	Ser	Gly	Ile	Ala	Ser	Gly	Gly	Arg	Leu	Tyr	Ile	Ser	Arg	
305					310				315				320			
atg	atg	cac	aaa	tct	tac	ata	gag	gtc	act	gag	gag	ggc	acc	gag	gct	1008
Met	Met	His	Lys	Ser	Tyr	Ile	Glu	Val	Thr	Glu	Glu	Gly	Thr	Glu	Ala	
					325			330				335				
act	gct	gcc	aca	gga	agt	aat	att	gta	gaa	aag	caa	ctc	cct	cag	tcc	1056
Thr	Ala	Ala	Thr	Gly	Ser	Asn	Ile	Val	Glu	Lys	Gln	Leu	Pro	Gln	Ser	
			340				345				350					
acg	ctg	ttt	aga	gct	gac	cac	cca	ttc	cta	ttt	gtt	atc	agg	aag	gat	1104
Thr	Leu	Phe	Arg	Ala	Asp	His	Pro	Phe	Leu	Phe	Val	Ile	Arg	Lys	Asp	
		355			360						365					
gac	atc	atc	tta	ttc	agt	ggc	aaa	gtt	tct	tgc	cct	tga				1143
Asp	Ile	Ile	Leu	Phe	Ser	Gly	Lys	Val	Ser	Cys	Pro					
		370			375					380						

<210> 2
<211> 380
<212> PRT
<213> Homo sapiens

<400> 2																
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Arg	Glu	Met	Asp	Asp	Asn	Gln	Gly	Asn	Gly	Asn	Val	Phe	Phe	Ser	Ser	
									25				30			
Leu	Ser	Leu	Phe	Ala	Ala	Leu	Ala	Leu	Val	Arg	Leu	Gly	Ala	Gln	Asp	
									40				45			
Asp	Ser	Leu	Ser	Gln	Ile	Asp	Lys	Leu	Leu	His	Val	Asn	Thr	Ala	Ser	
									55			60				
Gly	Tyr	Gly	Asn	Ser	Ser	Asn	Ser	Gln	Ser	Gly	Leu	Gln	Ser	Gln	Leu	
									65			75		80		
Lys	Arg	Val	Phe	Ser	Asp	Ile	Asn	Ala	Ser	His	Lys	Asp	Tyr	Asp	Leu	
									85			90		95		
Ser	Ile	Val	Asn	Gly	Leu	Phe	Ala	Glu	Lys	Val	Tyr	Gly	Phe	His	Lys	
									100			105		110		
Asp	Tyr	Ile	Glu	Cys	Ala	Glu	Lys	Leu	Tyr	Asp	Ala	Lys	Val	Glu	Arg	
									115			120		125		
Val	Asp	Phe	Thr	Asn	His	Leu	Glu	Asp	Thr	Arg	Arg	Asn	Ile	Asn	Lys	
									130			135		140		

b)

c)

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
145 . 150 155 160

Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
165 170 175

Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
180 185 190

Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
195 200 205

His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
210 215 220

Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
225 230 235 240

Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
245 250 255

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
260 265 270

Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
275 280 285

Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
290 295 300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
305 310 315 320

Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
325 330 335

Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
340 345 350

Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
355 360 365

Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro
370 375 380

b1
<210> 3
<211> 29
<212> DNA
<213> Artificial Sequence

c1
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<223> Description of Artificial Sequence:Artificially
synthesized degenerative primer sequence

<220>
<221> misc_feature

<222> 26, 29
<223> n is a or g or c or t.

<400> 3
tgtaatgctg tgtacttaaa ggcaantgn

29

<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
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<220>
<221> misc_feature
<222> 3, 9, 15
<223> n is a or g or c or t.

<400> 4
aanagraang grtcngc

17

<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized degenerative primer sequence

<220>
<221> misc_feature
<222> 6, 9, 12, 15, 18, 21
<223> n is a or g or c or t.

<400> 5
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26

<210> 6
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized degenerative primer sequence

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cgacctccag aggcaattcc agagagatca gccctgg

37

b1
C1 <210> 7

b1
C1

<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized degenerative primer sequence

<400> 7
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<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized antisense primer sequence

<400> 8
gctcaggca gtgaagatgc tcagggaga 30

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized antisense primer sequence

<400> 9
ctgacgtca cagtcaccc gaggacc 27

<210> 10
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized sense primer sequence

<400> 10
gaggtcttag aagaaggcac tgaggcaact gctgcc 36

<210> 11
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 11

Phe Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe
1 5 10 15

<210> 12

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 12

Ser Gln Ser Gly Leu Gln Ser Gln Leu Lys Arg Val Phe Ser Asp
1 5 10 15

<210> 13

<211> 16

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 13

Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu
1 5 10 15

<210> 14

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 14

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
1 5 10 15

<210> 15

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 15
Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser Thr Leu Phe Arg
1 5 10 15

<210> 16
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 16
Leu Gly Leu Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp
1 5 10

<210> 17
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially synthesized domain peptide of human megsin

<400> 17
Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser Thr Val
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<210> 18
<211> 1229
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (8)..(1147)

<220>
<221> misc_feature
<222> 158, 159, 160, 287, 288, 289
<223> n is a or g or c or t.

<300>
<310> PCT/JP98/04269
<311> 1998-09-22

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1 5 10

tta ttc aga gag atg gat agt caa gga aac gga aat gta ttc ttc 97

b1

c1

Leu Phe Arg Glu Met Asp Ser Ser Gln Gly Asn Gly Asn Val Phe Phe
 15 . 20 25 30

tct tcc ctg agc atc ttc act gcc ctg agc cta atc cgt ttg ggt gct 145
 Ser Ser Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala
 35 40 45

cga ggt gac tgt nnn cgt cag att gac aag gcc ctg cac ttt atc tcc 193
 Arg Gly Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser
 50 55 60

cca tca aga caa ggg aat tca tcg aac agt cag cta gga ctg caa tat 241
 Pro Ser Arg Gln Gly Asn Ser Asn Ser Gln Leu Gly Leu Gln Tyr
 65 70 75

caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag gat nnn 289
 Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa
 80 85 90

aaa ctc agc att gcc aat gga gtt ttt gca gag aaa gta ttt gat ttt 337
 Lys Leu Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe
 95 100 105 110

cat aag agc tat atg gag tgt gct gaa aac tta tac aat gct aaa gtg 385
 His Lys Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val
 115 120 125

gaa aga gtt gat ttt aca aat gat ata caa gaa acc aga ttt aaa att 433
 Glu Arg Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile
 130 135 140

aat aaa tgg att gaa aat gaa aca cat ggc aaa atc aag aag gtg ttg 481
 Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu
 145 150 155

ggg gac agc agc ctc agc tca tca gct gtc atg gtg cta gtg aat gct 529
 Gly Asp Ser Ser Leu Ser Ser Ala Val Met Val Leu Val Asn Ala
 160 165 170

gtt tac ttc aaa ggc aag tgg aaa tcg gcc ttc acc aag agt gat acc 577
 Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr
 175 180 185 190

ctc agt tgc cat ttc agg tct ccc agc ggt cct gga aaa gca gtt aat 625
 Leu Ser Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn
 195 200 205

atg atg cat caa gaa cgg agg ttc aat ttg tct acc att cag gag cca 673
 Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro
 210 215 220

cca atg cag att ctt gag cta caa tat cat ggt ggc ata agc atg tac 721
 Pro Met Gln Ile Leu Glu Leu Gln Tyr His Gly Gly Ile Ser Met Tyr
 225 230 235

atc atg ttg ccc gag gat gac cta tcc gaa att gaa agc aag ctg agt 769
 Ile Met Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser

240	245	250	
ttc cag aat cta atg gac tgg aca aat agc agg aag atg aaa tct cag Phe Gln Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln			817
255	260	265	270
tat gtg aat gtg ttt ctc ccc cag ttc aag ata gag aaa gat tat gaa Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu			865
275	280	285	
atg agg agc cac ttg aaa tct gta ggc ttg gaa gac atc ttt gtt gag Met Arg Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu			913
290	295	300	
tcc agg gct gat ctg tct gga att gcc tct gga ggt cgt ctc tat gta Ser Arg Ala Asp Ieu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val			961
305	310	315	
tca aag cta atg cac aag tcc ctc ata gag gtc tca gaa gaa ggc acc Ser Lys Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr			1009
320	325	330	
gag gca act gct gcc aca gaa agt aac atc gtt gaa aag cta ctt cct Glu Ala Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro			1057
335	340	345	350
gaa tcc acg gtg ttc aga gct gac cgc ccc ttt ctg ttt gtc att agg Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg			1105
355	360	365	
aag aat ggc atc atc tta ttt act ggc aaa gtc tcg tgt cct Lys Asn Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro			1147
370	375	380	
tgaaattcta ttgggtttc catacaactaa caggcatgaa gaaacatcat aagtgaatag			1207
aattgttaatt ggaagtacat gg			1229

<210> 19
 <211> 380
 <212> PRT
 <213> Rattus norvegicus

<220>
 <221> misc feature
 <222> 51, 94
 <223> Xaa is unknown.

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 20 25 30

Leu Ser Ile Phe Thr Ala Leu Ser Leu Ile Arg Leu Gly Ala Arg Gly

35	40	45	
Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser			
50	55	60	
Arg Gln Gly Asn Ser Ser Asn Ser Gln Leu Gly Leu Gln Tyr Gln Leu			
65	70	75	80
Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu			
85	90	95	
Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys			
100	105	110	
Ser Tyr Met Glu Cys Ala Glu Asn Leu Tyr Asn Ala Lys Val Glu Arg			
115	120	125	
Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys			
130	135	140	
Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp			
145	150	155	160
Ser Ser Leu Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr			
165	170	175	
Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser			
180	185	190	
Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met			
195	200	205	
His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met			
210	215	220	
Gln Ile Leu Glu Leu Gln Tyr His Gly Ile Ser Met Tyr Ile Met			
225	230	235	240
Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln			
245	250	255	
Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val			
260	265	270	
Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg			
275	280	285	
Ser His Leu Lys Ser Val Gly Leu Glu Asp Ile Phe Val Glu Ser Arg			
290	295	300	
Ala Asp Leu Ser Gly Ile Ala Ser Gly Arg Leu Tyr Val Ser Lys			
305	310	315	320
Leu Met His Lys Ser Leu Ile Glu Val Ser Glu Glu Gly Thr Glu Ala			
325	330	335	
Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser			

340 345 350

Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val Ile Arg Lys Asn		
355	360	365
Gly Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro		
370	375	380

<210> 20
<211> 1147
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1104)

<300>
<310> PCT/JP98/04269
<311> 1998-09-22

<400> 20

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1 5 10 15	

ttc ttc tct tcc ctg agc atc ttc act gcc ctg acc cta atc cgt ctg	96
Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu	
20 25 30	

ggt gct cga ggt gac tgt gca cgt cag att gac aag gca ctg cac ttt	144
Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe	
35 40 45	

aac ata cca tca aga caa gga aac tca tct aat aat cag cca gga ctt	192
Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu	
50 55 60	

cag tat caa ttg aaa aga gtt ctt gct gac ata aac tca tct cat aag	240
Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys	
65 70 75 80	

gat tat gaa ctc agc att gcc act gga gtt ttt gca gaa aaa gtc tat	288
Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr	
85 90 95	

gac ttt cat aag aac tac att gag tgt gct gaa aac tta tac aat gct	336
Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala	
100 105 110	

aaa gtg gaa aga gtt gac ttc aca aat gat gta caa gat acc aga ttt	384
Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe	
115 120 125	

aaa att aat aaa tgg att gaa aat gag aca cat gga aag atc aag aag	432
Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys	

130	135	140	
gtg ttg ggc gac agc agc ctc agc tcg tcg gct gtc atg gtg ctg gtg Val Leu Gly Asp Ser Ser Leu Ser Ser Ala Val Met Val Leu Val			
145	150	155	480
aac gct gtt tac ttc aaa ggc aaa tgg aaa tcg gcc ttc acc aag act Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr			
165	170	175	528
gat acc ctc agt tgc cgt ttt agg tct ccc acg tgt cct gga aaa gta Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val			
180	185	190	576
gtt aat atg atg cat caa gaa cgg cggtt aat ttg tct acc att cag Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln			
195	200	205	624
cag cca cca atg cag gtt ctt gag ctc caa tat cat ggt ggc ata agc Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser			
210	215	220	672
atg tac att atg ctg cct gag gat ggc cta tgt gaa att gaa agc aag Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys			
225	230	235	720
ctg agt ttc cag aat ctg atg gac tgg acc aat agg agg aaa atg aaa Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys			
245	250	255	768
tct cag tat gtg aac gtg ttt ctc ccc cag ttc aag ata gag aag aat Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn			
260	265	270	816
tat gaa atg acg cac cac ttg aaa tcc tta ggc ttg aaa gat atc ttt Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe			
275	280	285	864
gat gag tcc agt gca gat ctc tct gga att gcc tct gga ggt cgt ctc Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu			
290	295	300	912
tac gta tca aag cta atg cac aag tca ttc ata gag gtc tca gag gag Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu			
305	310	315	960
ggc act gaa gcc act gct gcc aca gaa aat aac att gtt gaa aag cag Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln			
325	330	335	1008
ctt cct gag tcc aca gtg ttc aga gcc gac cgc ccc ttt ctg ttt gtc Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val			
340	345	350	1056
atc aag aag aat gac atc atc tta ttt act ggc aaa gtc tct tgt cct Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro			
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Phe Phe Ser Ser Leu Ser Ile Phe Thr Ala Leu Thr Leu Ile Arg Leu
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Gly Ala Arg Gly Asp Cys Ala Arg Gln Ile Asp Lys Ala Leu His Phe
35 40 45

Asn Ile Pro Ser Arg Gln Gly Asn Ser Ser Asn Asn Gln Pro Gly Leu
50 55 60

Gln Tyr Gln Leu Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys
65 70 75 80

Asp Tyr Glu Leu Ser Ile Ala Thr Gly Val Phe Ala Glu Lys Val Tyr
85 90 95

Asp Phe His Lys Asn Tyr Ile Glu Cys Ala Glu Asn Leu Tyr Asn Ala
100 105 110

Lys Val Glu Arg Val Asp Phe Thr Asn Asp Val Gln Asp Thr Arg Phe
115 120 125

Lys Ile Asn Lys Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys
130 135 140

Val Leu Gly Asp Ser Ser Leu Ser Ser Ala Val Met Val Leu Val
145 150 155 160

Asn Ala Val Tyr Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Thr
165 170 175

Asp Thr Leu Ser Cys Arg Phe Arg Ser Pro Thr Cys Pro Gly Lys Val
180 185 190

Val Asn Met Met His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln
195 200 205

Gln Pro Pro Met Gln Val Leu Glu Leu Gln Tyr His Gly Gly Ile Ser
210 215 220

Met Tyr Ile Met Leu Pro Glu Asp Gly Leu Cys Glu Ile Glu Ser Lys
225 230 235 240

Leu Ser Phe Gln Asn Leu Met Asp Trp Thr Asn Arg Arg Lys Met Lys
245 250 255

Ser Gln Tyr Val Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asn
260 265 270

Tyr Glu Met Thr His His Leu Lys Ser Leu Gly Leu Lys Asp Ile Phe
275 280 285

Asp Glu Ser Ser Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu
290 295 300

Tyr Val Ser Lys Leu Met His Lys Ser Phe Ile Glu Val Ser Glu Glu
305 310 315 320

Gly Thr Glu Ala Thr Ala Ala Thr Glu Asn Asn Ile Val Glu Lys Gln
325 330 335

Leu Pro Glu Ser Thr Val Phe Arg Ala Asp Arg Pro Phe Leu Phe Val
340 345 350

Ile Lys Lys Asn Asp Ile Ile Leu Phe Thr Gly Lys Val Ser Cys Pro
355 360 365

b1
c1
conclu